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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2009; month=5; day=4; hr=19; min=35; sec=18; ms=596;]

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Application No: 10726615 Version No: 1.0

Input Set:

Output Set:

Started: 2009-04-27 16:20:45.901
Finished: 2009-04-27 16:20:45.952
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 51 ms
Total Warnings: 0
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No. of SeqIDs Defined: 1
Actual SeqID Count: 1

SEQUENCE LISTING

<110> Rangnekar, Vivek M.

<120> Identificatin of a unique core domain of par-4 sufficient for
selective apoptosis induction in cancer cells

<130> 104072.B000118

<140> 10726615

<141> 2009-04-27

<150> 60/430,669

<151> 2002-12-04

<160> 1

<170> PatentIn version 3.5

<210> 1

<211> 332

<212> PRT

<213> Rattus norvegicus

<400> 1

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20 25 30

Gly Pro Gly Ser Ser Gly Gly Asp Pro Ala Ala Lys Ser Pro Ala Gly
35 40 45

Pro Leu Ala Gln Thr Thr Ala Ala Gly Thr Ser Glu Leu Asn His Gly
50 55 60

Pro Ala Gly Ala Ala Ala Pro Ala Ala Pro Gly Pro Gly Ala Leu Asn
65 70 75 80

Cys Ala His Gly Ser Ser Ala Leu Pro Arg Gly Ala Pro Gly Gly Ser
85 90 95

Arg Arg Pro Glu Asp Glu Cys Pro Ile Ala Ala Gly Ala Ala Gly Ala
100 105 110

Pro Ala Ser Arg Gly Asp Glu Glu Glu Pro Asp Ser Ala Pro Glu Lys
115 120 125

Gly Arg Ser Ser Gly Pro Ser Ala Arg Lys Gly Lys Gly Gln Ile Glu
130 135 140

Lys Arg Lys Leu Arg Glu Lys Arg Arg Ser Thr Gly Val Val Asn Ile
145 150 155 160

Pro Ala Ala Glu Cys Leu Asp Glu Tyr Glu Asp Asp Glu Ala Gly Gln
165 170 175

Lys Glu Arg Lys Arg Glu Asp Ala Ile Thr Gln Gln Asn Thr Ile Gln
180 185 190

Asn Glu Ala Ala Ser Leu Pro Asp Pro Gly Thr Ser Tyr Leu Pro Gln
195 200 205

Asp Pro Ser Arg Thr Val Pro Gly Arg Tyr Lys Ser Thr Ile Ser Ala
210 215 220

Pro Glu Glu Glu Ile Leu Asn Arg Tyr Pro Arg Thr Asp Arg Ser Gly
225 230 235 240

Phe Ser Arg His Asn Arg Asp Thr Ser Ala Pro Ala Asn Phe Ala Ser
245 250 255

Ser Ser Thr Leu Glu Lys Arg Ile Glu Asp Leu Glu Lys Glu Val Leu
260 265 270

Arg Glu Arg Gln Glu Asn Leu Arg Leu Thr Arg Leu Met Gln Asp Lys
275 280 285

Glu Glu Met Ile Gly Lys Leu Lys Glu Glu Ile Asp Leu Leu Asn Arg
290 295 300

Asp Leu Asp Asp Met Glu Asp Glu Asn Glu Gln Leu Lys Gln Glu Asn
305 310 315 320

Lys Thr Leu Leu Lys Val Val Gly Gln Leu Thr Arg
325 330